REMARKS

Applicant believes no new matter is added by these amendments to the claims.

Amendments to the claims.

Claims 1-21, 23, 34-35 and 39-40 are canceled in this amendment. Claims 22, 24-32, 36-37, and 41-42 are presently amended. New claims 43-44 are added by this amendment. After entry of this amendment, claims 22, 24-33, 36-38 and 41-44 will remain in this application.

Support for the following language in the claims may be found in the specification, for example:

for stringent conditions comprising 6X SSC at 65° C and two wash steps of 10 to 30 minutes of about 0.2x SSC, 0.1% SDS at 65°C or 0.1x SSC, 0.1% SDS at 65°C, on page 42, line 33 to page 43, line 13;

for "65%", 90% and "95%" identity for a conserved domain of the invention on page 14, line 33 to page 15, line 3, on page 36, lines 28-32, and on page 29, Table 1, row "14...G3456" lists the "% ID to Second Conserved Domain of G1073" as "65%";

for a "recombinant construct comprising a nucleic acid" at page 52, lines 7-8 and on page 78, line 32; and

for "expression of the AT-hook transcription factor polypeptide is regulated by a constitutive, inducible, or tissue-specific promoter" on page 53, lines 2-4 and 21-25, and claim 14(a) as filed.

Response to claim objections, double patenting and rejections.

Item 5. Claim objections

Claims 22, 27, 32 and 37 have been amended by incorporating the claim element --the AT-hook transcription factor polypeptide comprises a conserved domain that is at least 65% or 90% identical in its amino acid sequence to amino acids 106-201 of SEQ ID NO: 14--. Dependent claims 25, 30, 36 and 41, each comprise a claim element of even greater percentage identity to amino acids 106-201 of SEQ ID NO: 14 than their respective independent claims, and are thus more limited.

Accordingly, Applicant believes that the present objections to claims 25, 30, 36 and 41 have been overcome.

Item 7. Obvious-type double patenting with respect to U.S. Patent No. 6,717,034

A terminal disclaimer was submitted on 9 January 2008 which Applicant believes overcomes the double patenting rejection. Accordingly, Applicant respectfully requests that this rejection be withdrawn.

Item 8. Provisional obvious-type double patenting with respect to Application No. 10/870,198

A terminal disclaimer was submitted on 9 January 2008 which Applicant believes overcomes the provisional double patenting rejection. Accordingly, Applicant respectfully requests that this rejection be withdrawn.

Item 9. Provisional double patenting with respect to Application No. 11/435,388

For Application No. 11/435,388, Applicant has responded to a restriction requirement and elected polynucleotide or polypeptide inventions corresponding to transcription factors with the AP2 family. As such, Applicant believes that the transgenic plants and methods in the claims of Application No. 11/435,388 are distinct from the instant claims.

Applicant will address this rejection at a later date if the elected sequences for Application No. 11/435,388 are, in the opinion of the Examiner, sufficiently similar to the present SEQ ID NOs. 13 and 14 to maintain this rejection.

Item 11. Rejection under 35 USC 112, first paragraph, written description

The presently amended independent claims comprise the element of a conserved domain that is at least *65%* identical to amino acids 106-201 of SEQ ID NO: 14. On page 29, Table 1, row "14...G3456" lists the "% ID to Second Conserved Domain of G1073" as "65%". See also page 14, line 33 to page 15, line 1, for example.

Accordingly, Applicant respectfully requests that this rejection be withdrawn.

Item 12. Rejection under 35 USC 112, first paragraph, written description

Applicant believes the rejection of the claims under 35 U.S.C. §112, first paragraph, written description, is avoided by the amendment of the claims for the reasons set forth below.

The specification provides multiple working examples, and the breadth of the instant claims is narrower than exemplary claims in the *Written Description Training Materials*.

The claimed hybridization conditions include two wash steps of 10 to 30 minutes with about 0.2x SSC, 0.1% SDS at 65° C. These conditions are more stringent than the exemplary wash conditions provided in the *Written Description Training Materials*, Rev. 1, March 25, 2008, Example 6, which include a lower stringency first wash step for 10 minutes at about 42°C with about 20% formamide in 0.1X SSC. Example 6 in the Training Materials provides an actual reduction to practice for and the complete chemical structure of only one species of the claimed genus of nucleic acids. In the specification, Applicant provided the structure of a considerable number of closely related At-hook

transcription factor polypeptides that function similarly by conferring increased tolerance to water deficit and/or increased biomass in plants. The specification thus discloses other nucleic acids that both hybridize to the complement of SEQ ID NO: 13 and encode polypeptides that confer greater water deficit tolerance and/or biomass. G1073 and the other related sequences listed in Table 1 of the declaration by Dr. Ratcliffe are predicted to hybridize with the G3456 DNA sequence under even conditions less stringent than those being claimed, as shown in Exhibit C, previously submitted.

Because hybridization under highly stringent conditions requires a high degree of structural complementarity, nucleic acids that hybridize to the complement of SEQ ID NO: 1 must share many nucleotides in common with SEQ ID NO: 13. Thus, the claimed genus necessarily includes partial structures of SEQ ID NO: 13. The disclosure of SEQ ID NO: 13 and closely related sequences that function in the same manner, combined with the knowledge in the art regarding hybridization would put one in possession of the genus of nucleic acids that would hybridize under stringent conditions to SEQ ID NO: 13.

Sequences closely related to SEQ ID NO: 14 conferred increased water deficit tolerance and biomass.

As to function of these sequences, please see the declaration by Dr. Ratcliffe, which shows that sequences closely related to G3456, SEQ ID NO: 14, were tested in plants and conferred the traits of increased water deficit tolerance. G1073, SEQ ID NO: 2, has also shown its ability to make plants more tolerant to water deficit, (e.g., see Figures 8A and 8B of the present specification). On page 61, lines 8-13, Applicant also disclosed that *Arabidopsis* plants transformed with *Arabidopsis thaliana* polypeptides G1073, G1067, G2153 and G2156, *Oryza sativa* polypeptides G3399 and G3407, and *Glycine max* polypeptides G3456, G3459 and G3460, become larger than controls (SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, and 18, respectively) became larger than controls. G2153 was also tested in tomato plants, and "[t]omato plants overexpressing the *A. thaliana* G2153 polypeptide have been found to be larger and produce more fruit than wild-type control tomato plants" (page 61, lines 17-18). Applicant's patent application 10/870,198 (e.g., on page 60, lines 23 of the 10/870,198 specification) also shows that G3401, SEQ ID NO: 38 of the present specification, can be used to make larger plants. Applicant described how candidate paralogous and orthologous sequences were identified among *Arabidopsis* transcription factors through alignment, identity, and phylogenic relationships, and for orthologs, using reciprocal comparisons (e.g., page 96, lines 4-10). The tested sequences derive from diverse plant species including eudicots and, in the case of G3401, SEQ ID NO: 38, a monocot. Thus, nature has preserved both the structure of the second conserved domain and the functions of sequences that possess this domain and that

were found using Applicant's description.

There is a correlation between structure and function.

There is an art-recognized correlation between structure and DNA binding and regulatory function of At-hook domains.

A recognizable second conserved domain similar to amino acids 106-201 of SEQ ID NO: 14 is found in every transcription factor sequence, as shown in the column "Second Conserved Domain" in Table 1 of the specification. See also, for example, the second conserved domains spanning Figures 5E through 5G for a number of homologs closely-related to G3456, SEQ ID NO: 14. As the functions of conferring greater water deficit tolerance and biomass are associated with these sequences, these second conserved domains, including those with at least 65% (in the claims also directed to hybridization conditions), or 90%, or 95% identity in their amino acid sequences to amino acids 106-201 of SEQ ID NO: 14, are also highly correlated with these functions.

Further with regard to the second conserved domains of G3456-related proteins and their relationship to the function of the encompassed proteins, the Enzo court (Enzo Biochem, Inc. v. Gen-Probe Inc., 296 F.3d 1316, 63 USPQ2d 1609 (Fed. Cir. 2002)) adopted the standard that "the written description requirement can be met by 'showing that an invention is complete by disclosure of sufficiently detailed, relevant identifying characteristics . . . i.e., complete *or partial structure*, other physical and/or chemical properties, functional characteristics when coupled with a known or *disclosed correlation between function and structure*, or some combination of such characteristics'" Id. at 1324, 63 USPQ2d at 1613 (*emphasis* added).

The specification discloses known or disclosed correlation between structure and function by describing the At-hook domains and transcriptional regulatory activity of the disclosed sequences, and another partial structure of G3456 (i.e., the "second conserved domain" of SEQ ID NO: 14), and other relevant identifying characteristics of the protein (e.g., its ability to bind DNA, its ability to confer increased water deficit tolerance or biomass), as well as a list of functional and related molecular species that have recognizable At-hook and second conserved domains within certain hybridization stringency or percent identity guidelines. The specification also discloses methods for identifying related polypeptides, and working examples in which G3456 and other closely related proteins are successfully isolated and tested using the disclosed methods. Thus, those of ordinary skill in the art of isolating proteins would recognize the inventor to have been in possession of the claimed protein at the time of filing based on these identifying characteristics and the disclosed isolation method (see *Written Description Training Materials*, Example 5).

There is thus a very high correlation between sequences comprise the claimed structure and that function or are expected to function as claimed. Exhibit C attached to the declarations submitted 9 January 2008 shows that five of six sequences tested (G3456, SEQ ID NO: 14; G3460, SEQ ID NO: 18; G3459, SEQ ID NO: 16; G2153, SEQ ID NO: 6; G3401, SEQ ID NO: 38) do, in fact, perform the claimed function by conferring greater tolerance to water deficit, and five of six plants tested also confer increased plant biomass (the six sequence, G3457, has not yet been fully tested; for example, no soil-based drought assays have yet been performed). Transformed plants expressing five closely related transcription factor sequences with closely related second conserved domains tested in a full range of water deficit assays confer the claimed functions, establishing a strong disclosed correlation between function and structure.

Accordingly, Applicant respectfully requests that this rejection be withdrawn.

Item 15. Rejection under 35 USC 102/103

The presently amended claims include the claim element of a polypeptide that comprises a conserved domain that has at least 65% or greater identity to amino acids 106-201 of SEQ ID NO: 14.

An alignment of the Weigel sequence and amino acids 106-201 of SEQ ID NO: 14 (see below) shows that the two subsequences are, in fact, only 61.9% identical in their amino acid residues. Thus, the Weigel reference, lacking the claimed second conserved domain, does not anticipate the present claims and should not be combined with any other reference to form the basis of an obviousness rejection.

Alignment of G3456 and G1067 (Escarola) second conserved domains
Identities = 65/105 (61.9%)

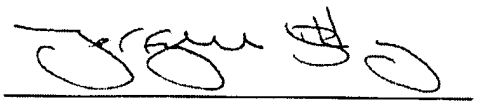
```
G3456:      VAQFARRRQRGVSILSGSGTVVNVNLRQPTAPG---------AVMALHGRFDILSLTGSF
            V   ARRR RGVS L G GTV NV LRQP  PG          V  LHGRF ILSLTG
G1067:      VSTYARRRGRGVSVLGGNGTVSNVTLRQPVTPGNGGGVSGGGGVVTLHGRFEILSLTGTV

G3456:      LPGPSPPGATGLTIYLAGGQGQIVGGEVVGPLVAAGPVLVMAATF
            LP P PPGA GL I LAGGQGQ VGG VV PL A  PV  MAA F
G1067:      LPPPAPPGAGGLSIFLAGGQGQVVGGSVVAPLIASAPVILMAASF
```

Accordingly, Applicant respectfully requests that this rejection be withdrawn.

CONCLUSION

Applicant believes that no additional fee is due with this communication. However, if the USPTO determines that a fee is due, the Commissioner is hereby authorized to charge Mendel Biotechnology, Inc. Deposit Account No. **50-1025.**

Respectfully submitted,
MENDEL BIOTECHNOLOGY, INC.



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